



# SEQUENCE LISTING

<110> Yumin, Tao  
Gordon-Kamm, William  
Shen, Bo  
Lowe, Keith  
Danilevskaya, Olga  
Mahajan, Pramod  
Rafalski, Jan Antoni  
Sakai, Hajime  
Klein, Theodore

<120> Transcriptional Regulatory Nucleic  
Acids, Polypeptides, and Methods of Use Thereof

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<151> 2001-12-04

<150> 60/251,555

<151> 2000-12-06

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Glu Arg Leu Leu Asp Arg Asp Gln Val Asp Gly Asp Glu Ser Val Glu	
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 gat gaa gaa gaa gat gga ttc tta aaa gga ttc aag gtt gca aac ttt	143
Asp Glu Glu Glu Asp Gly Phe Leu Lys Gly Phe Lys Val Ala Asn Phe	
35 40 45	
 gaa tat atc gat gag gca aag gct cag gca gaa aaa gag gag gca cgg	191
Glu Tyr Ile Asp Glu Ala Lys Ala Gln Ala Glu Lys Glu Glu Ala Arg	
50 55 60	

aga aag gct gca gct gag gct gaa aat tct gaa aga aac tac tgg gat Arg Lys Ala Ala Ala Glu Ala Glu Asn Ser Glu Arg Asn Tyr Trp Asp 65 70 75	239
gaa cta ttg aag gat aga tat gat gta cag aaa gtt gaa gaa cat act Glu Leu Leu Lys Asp Arg Tyr Asp Val Gln Lys Val Glu Glu His Thr 80 85 90 95	287
gct atg gga aaa ggg aaa aga agc cgc aaa cag atg gct gcc gct gat Ala Met Gly Lys Gly Lys Arg Ser Arg Lys Gln Met Ala Ala Ala Asp 100 105 110	335
gaa gat gac att cat gat tta agt tcc gaa gat gag gat tac tca ttg Glu Asp Asp Ile His Asp Leu Ser Ser Glu Asp Glu Asp Tyr Ser Leu 115 120 125	383
gag gat gac att tca gat aat gac aca agt ttg caa gga aat att tct Glu Asp Asp Ile Ser Asp Asn Asp Thr Ser Leu Gln Gly Asn Ile Ser 130 135 140	431
ggg aag agg gga caa tat tct aag aga aaa tca cgt aat gtt gat tct Gly Lys Arg Gly Gln Tyr Ser Lys Arg Lys Ser Arg Asn Val Asp Ser 145 150 155	479
att cca ttg atg gag ggc gaa gga cgt acc ttg aga gtt ctt gga ttc Ile Pro Leu Met Glu Gly Glu Gly Arg Thr Leu Arg Val Leu Gly Phe 160 165 170 175	527
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ttt cag aat tat gac tgg aaa gag tat ctt cct cgt ctt aaa gga aaa Phe Gln Asn Tyr Asp Trp Lys Glu Tyr Leu Pro Arg Leu Lys Gly Lys 195 200 205	623
agt gtc gag gaa atc cag aga tat gct gaa ctt gtc atg gca cat ctt Ser Val Glu Glu Ile Gln Arg Tyr Ala Glu Leu Val Met Ala His Leu 210 215 220	671
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ctt atc gag gag aag atg gct gcc aca gga cca gga aaa att aca aac Leu Ile Glu Glu Lys Met Ala Ala Thr Gly Pro Gly Lys Ile Thr Asn 260 265 270	815
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aga ata tgg aaa gcg gag cat gat cta ctg tta ctg aga ggc ata ctg Arg Ile Trp Lys Ala Glu His Asp Leu Leu Leu Leu Arg Gly Ile Leu 290 295 300	911
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gtc gag gcc tta cga cca cac caa aat ggt act gcc agt gcc atc aaa Val Glu Ala Leu Arg Pro His Gln Asn Gly Thr Ala Ser Ala Ile Lys 500 505 510	1535

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Arg Arg Leu Arg Ala Glu Gly His Arg Val Leu Leu Phe Ala Gln Met
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act aaa atg ttg gac att ctt gag gat tac atg aat ttc aga aaa ttc      152
Thr Lys Met Leu Asp Ile Leu Glu Asp Tyr Met Asn Phe Arg Lys Phe
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aag tat ttc aga ctt gat ggg tct tca gcc atc tca gac cgc cgt gac      200
Lys Tyr Phe Arg Leu Asp Gly Ser Ser Ala Ile Ser Asp Arg Arg Asp
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atg gtc cga gat ttt cag aac agg aat gac ata ttt gtt ttc ttg tta      248
Met Val Arg Asp Phe Gln Asn Arg Asn Asp Ile Phe Val Phe Leu Leu
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agc aca aga gct ggg ggg ctt ggt att aat ttg act gct gct gat act      296
Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Thr Ala Ala Asp Thr
                      70                      75                      80

gtt att ttt tat gaa att gac tgg aat cca aca caa gac cag cag gca      344
Val Ile Phe Tyr Glu Ile Asp Trp Asn Pro Thr Gln Asp Gln Gln Ala
      85                      90                      95

atg gat aga aca cac aga ctt ggt caa aca aag gag gta act gtg tac      392
Met Asp Arg Thr His Arg Leu Gly Gln Thr Lys Glu Val Thr Val Tyr
      100                      105                      110                      115

agg ctt ata tgc aaa gat acc att gag gag aaa ata ttg caa aga gca      440
Arg Leu Ile Cys Lys Asp Thr Ile Glu Glu Lys Ile Leu Gln Arg Ala
                      120                      125                      130

aag cag aaa aat gca gtg caa gag tta gtt atg aag ggg aaa cat gtc      488
Lys Gln Lys Asn Ala Val Gln Glu Leu Val Met Lys Gly Lys His Val
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gaa gga gat ttg acg ctc gaa gac ttg gat gat gct act gca gaa gct Glu Gly Asp Leu Thr Leu Glu Asp Leu Asp Asp Ala Thr Ala Glu Ala 200 205 210	680
gta gat caa gac aaa acg acc agc aaa aag aaa aag agc tcc cac aag Val Asp Gln Asp Lys Thr Thr Ser Lys Lys Lys Ser Ser His Lys 215 220 225	728
aaa cat acg aat act cat gat aat gac aat ata gac aag aat gga gag Lys His Thr Asn Thr His Asp Asn Asp Asn Ile Asp Lys Asn Gly Glu 230 235 240	776
gcc gat gtg gga gat cat ccg ggg agt agt aac aca gaa aac gaa cag Ala Asp Val Gly Asp His Pro Gly Ser Ser Asn Thr Glu Asn Glu Gln 245 250 255	824
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act gat gac aag gaa cta gct gct gct gcg gat cat gag aaa ccg gta Thr Asp Asp Lys Glu Leu Ala Ala Ala Ala Asp His Glu Lys Pro Val 280 285 290	920
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 Thr Val Tyr Arg Leu Ile Cys Lys Asp Thr Ile Glu Glu Lys Ile Leu  
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 Gln Arg Ala Lys Gln Lys Asn Ala Val Gln Glu Leu Val Met Lys Gly  
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 Lys His Val Gln Asp Asp His Leu Met Arg Gln Glu Asp Val Val Ser  
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 Ala Glu Ala Val Asp Gln Asp Lys Thr Thr Ser Lys Lys Lys Lys Ser  
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 Ser His Lys Lys His Thr Asn Thr His Asp Asn Asp Asn Ile Asp Lys  
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 Asn Gly Glu Ala Asp Val Gly Asp His Pro Gly Ser Ser Asn Thr Glu  
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 Asn Glu Gln Met Pro Glu Ser Arg Pro Lys Arg Ser Lys Arg Leu Met  
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 Lys Ser Ile Thr Asp Asp Lys Glu Leu Ala Ala Ala Ala Asp His Glu  
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cgt cca gaa gag agg aag ctt tta agg gaa aag aat ttt gat gga ttg 143

Arg Pro Glu Glu Arg Lys Leu Leu Arg Glu Lys Asn Phe Asp Gly Leu

35 40 45

caa ttt aat gtt ttg ctc acg cat tat gac ttg ata ctg aaa gat aag 191

Gln Phe Asn Val Leu Leu Thr His Tyr Asp Leu Ile Leu Lys Asp Lys

50 55 60

aag ttc cta aag aaa gtt cac tgg cat tat ttg att gtt gat gaa gga 239

Lys Phe Leu Lys Lys Val His Trp His Tyr Leu Ile Val Asp Glu Gly

65 70 75

cat cgt ctg aaa aat cat gaa tgt gct ctt gct cgc aca cta gtt tca 287

His Arg Leu Lys Asn His Glu Cys Ala Leu Ala Arg Thr Leu Val Ser

80 85 90 95

gga tat cag atc cgc cgc aga cta ctt tta act ggc act cca atc caa 335

Gly Tyr Gln Ile Arg Arg Arg Leu Leu Leu Thr Gly Thr Pro Ile Gln

100 105 110

aat agc cta caa gaa ctg tgg tct ttg ctt aac ttt att ctg ccc aat 383

Asn Ser Leu Gln Glu Leu Trp Ser Leu Leu Asn Phe Ile Leu Pro Asn

115 120 125

att ttt aat tca tct cag aat ttt gag gaa tgg ttt aat gca cca ttt 431

Ile Phe Asn Ser Ser Gln Asn Phe Glu Glu Trp Phe Asn Ala Pro Phe

130 135 140

gca tgt gat gtt agt ctt aat gat gag gaa cag cta tta atc ata cat 479

Ala Cys Asp Val Ser Leu Asn Asp Glu Glu Gln Leu Leu Ile Ile His

145 150 155

cgt ctg cat caa gtt ttg cgt cca ttt ttg ctg agg agg aaa aaa gat 527

Arg Leu His Gln Val Leu Arg Pro Phe Leu Leu Arg Arg Lys Lys Asp

160 165 170 175

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260 265 270	
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Glu Ile Tyr Leu Gln Met Tyr Asn Phe Lys Tyr Met Arg Leu Asp Gly	
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Ser Thr Lys Thr Glu Glu Arg Gly Arg Leu Leu Ala Asp Phe Asn Lys	
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Asp Trp Asn Pro Gln Met Asp Gln Gln Ala Glu Asp Arg Ala His Arg	
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Pro Leu Lys Lys Arg Ser Trp Thr Val Gln Asn Lys Arg Trp Val Ser	
385 390 395	

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1913

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Pro Glu Glu Arg Lys Leu Leu Arg Glu Lys Asn Phe Asp Gly Leu Gln  
35 40 45  
Phe Asn Val Leu Leu Thr His Tyr Asp Leu Ile Leu Lys Asp Lys Lys  
50 55 60  
Phe Leu Lys Lys Val His Trp His Tyr Leu Ile Val Asp Glu Gly His  
65 70 75 80  
Arg Leu Lys Asn His Glu Cys Ala Leu Ala Arg Thr Leu Val Ser Gly  
85 90 95  
Tyr Gln Ile Arg Arg Arg Leu Leu Leu Thr Gly Thr Pro Ile Gln Asn  
100 105 110  
Ser Leu Gln Glu Leu Trp Ser Leu Leu Asn Phe Ile Leu Pro Asn Ile  
115 120 125  
Phe Asn Ser Ser Gln Asn Phe Glu Glu Trp Phe Asn Ala Pro Phe Ala  
130 135 140  
Cys Asp Val Ser Leu Asn Asp Glu Glu Gln Leu Leu Ile Ile His Arg  
145 150 155 160  
Leu His Gln Val Leu Arg Pro Phe Leu Leu Arg Arg Lys Lys Asp Glu  
165 170 175  
Val Glu Lys Tyr Leu Pro Val Lys Thr Gln Val Ile Leu Lys Cys Asp  
180 185 190  
Met Ser Ala Trp Gln Lys Ala Tyr Tyr Glu Gln Val Thr Ser Arg Glu  
195 200 205  
Lys Val Ala Leu Gly Phe Gly Leu Arg Ser Lys Ala Leu Gln Asn Leu  
210 215 220  
Ser Met Gln Leu Arg Lys Cys Cys Asn His Pro Tyr Leu Phe Val Glu  
225 230 235 240  
His Tyr Asn Met Tyr Gln Arg Glu Glu Ile Val Arg Ala Ser Gly Lys  
245 250 255  
Phe Glu Leu Leu Asp Arg Leu Leu Pro Lys Leu Gln Arg Ala Gly His  
260 265 270  
Arg Val Leu Leu Phe Ser Gln Met Thr Lys Leu Leu Asp Val Leu Glu  
275 280 285  
Ile Tyr Leu Gln Met Tyr Asn Phe Lys Tyr Met Arg Leu Asp Gly Ser  
290 295 300  
Thr Lys Thr Glu Glu Arg Gly Arg Leu Leu Ala Asp Phe Asn Lys Lys  
305 310 315 320  
Asp Ser Glu Tyr Phe Met Phe Leu Leu Ser Thr Arg Ala Gly Gly Leu  
325 330 335  
Gly Leu Asn Leu Gln Thr Ala Asp Thr Val Ile Ile Phe Asp Ser Asp  
340 345 350  
Trp Asn Pro Gln Met Asp Gln Gln Ala Glu Asp Arg Ala His Arg Ile



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<400> 12
ttagaatggtt gggcgccctc t                                     21

<210> 13
<211> 1463
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (3)...(1460)

<221> misc_feature
<222> (0)...(0)
<223> n = A, T, C, or G; Xaa = Any Amino Acid

<400> 13
gt cga ccc acg cgt ccg cca gaa gag cgg aac cat ata agg gac aat      47
  Arg Pro Thr Arg Pro Pro Glu Glu Arg Asn His Ile Arg Asp Asn
    1             5             10             15

ttg ctg caa cct ggg aaa ttt gat gtg tgt gtg act agt ttt gaa atg      95
Leu Leu Gln Pro Gly Lys Phe Asp Val Cys Val Thr Ser Phe Glu Met
          20             25             30

gca atc aaa gaa aaa tct gcg ttg agg cgc ttc agc tgg cgc tac ata      143
Ala Ile Lys Glu Lys Ser Ala Leu Arg Arg Phe Ser Trp Arg Tyr Ile
          35             40             45

atc att gat gaa gct cac cgg ata aaa aat gaa aat tct ctt cta tca      191
Ile Ile Asp Glu Ala His Arg Ile Lys Asn Glu Asn Ser Leu Leu Ser
          50             55             60

aag act atg agg att tac aac act aat tat cgt ctc ctc atc aca ggc      239
Lys Thr Met Arg Ile Tyr Asn Thr Asn Tyr Arg Leu Leu Ile Thr Gly
          65             70             75

act cca ctc cag aat aat ctc cat gag ctc tgg gct ctc ctc aat ttc      287
Thr Pro Leu Gln Asn Asn Leu His Glu Leu Trp Ala Leu Leu Asn Phe
          80             85             90             95

ttg cta cct gaa ata ttt agc tct gcg gag acc ttt gat gaa tgg ttt      335
Leu Leu Pro Glu Ile Phe Ser Ser Ala Glu Thr Phe Asp Glu Trp Phe
          100             105             110

caa ata tct ggg gaa aat gat caa cag gag gtg gtg cag cag ctt cat      383
Gln Ile Ser Gly Glu Asn Asp Gln Gln Glu Val Val Gln Gln Leu His
          115             120             125

aag gtt ctt cgc cca ttc ctt ctt agg agg ctc aag tct gat gta naa      431
Lys Val Leu Arg Pro Phe Leu Leu Arg Arg Leu Lys Ser Asp Val Xaa
          130             135             140

aag ggc cta cct cca aag aaa gaa aca att ctt aaa gtt gga atg tct      479
Lys Gly Leu Pro Pro Lys Lys Glu Thr Ile Leu Lys Val Gly Met Ser

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145	150	155	
cag atg caa aag cag tac tat cgt gct ctg ctt cag aag gat ttg gag Gln Met Gln Lys Gln Tyr Tyr Arg Ala Leu Leu Gln Lys Asp Leu Glu 160 165 170 175			527
gtt att aat gct ggt ggt gaa cgc aag cga ttg ctt aac att gcc atg Val Ile Asn Ala Gly Gly Glu Arg Lys Arg Leu Leu Asn Ile Ala Met 180 185 190			575
cag ttg cgc aag tgc tgc aac cat cca tat tta ttc caa gga gct gaa Gln Leu Arg Lys Cys Cys Asn His Pro Tyr Leu Phe Gln Gly Ala Glu 195 200 205			623
cct ggg cca ccc tac aca act ggt gaa cat cta att gag aat gca gga Pro Gly Pro Pro Tyr Thr Thr Gly Glu His Leu Ile Glu Asn Ala Gly 210 215 220			671
aaa atg gtt cta ctt gat aaa ttg ctg ccc aag cta aag gag cgt gat Lys Met Val Leu Leu Asp Lys Leu Leu Pro Lys Leu Lys Glu Arg Asp 225 230 235			719
tcc aga gtc ctt att ttt tca cag atg acc agg ctt ttg gat atc ttg Ser Arg Val Leu Ile Phe Ser Gln Met Thr Arg Leu Leu Asp Ile Leu 240 245 250 255			767
gaa gat tat ctt atg tat agg gga tat cag tat tgt cga att gat gga Glu Asp Tyr Leu Met Tyr Arg Gly Tyr Gln Tyr Cys Arg Ile Asp Gly 260 265 270			815
aat aca ggt gga gaa gat cgt gat gca tcc att gaa gcc ttc aat agt Asn Thr Gly Gly Glu Asp Arg Asp Ala Ser Ile Glu Ala Phe Asn Ser 275 280 285			863
cca gga agt gag aag ttt gtt ttc tta ctt tca act agg gca ggt ggc Pro Gly Ser Glu Lys Phe Val Phe Leu Leu Ser Thr Arg Ala Gly Gly 290 295 300			911
ctt ggt atc aac ttg gcc act gct gat gtt gtg gtt ctc tat gac agc Leu Gly Ile Asn Leu Ala Thr Ala Asp Val Val Val Leu Tyr Asp Ser 305 310 315			959
gat tgg aat ccc caa gct gat ctg caa gct cag gac cgt gca cat aga Asp Trp Asn Pro Gln Ala Asp Leu Gln Ala Gln Asp Arg Ala His Arg 320 325 330 335			1007
ata ggt caa aaa gaa aga agt tca agt gtt ccg ctt ttg cac ttg agt Ile Gly Gln Lys Glu Arg Ser Ser Ser Val Pro Leu Leu His Leu Ser 340 345 350			1055
tca act att gag gaa aag gtg att gag aga gca tat aag aag cta gca Ser Thr Ile Glu Glu Lys Val Ile Glu Arg Ala Tyr Lys Lys Leu Ala 355 360 365			1103
ttg gat gct ttg gtt att cag caa gga cga ttg gca gag cag aaa act Leu Asp Ala Leu Val Ile Gln Gln Gly Arg Leu Ala Glu Gln Lys Thr			1151

370	375	380	
gtc aat aag gat gat ctt ctg caa atg gtg cgg ttt ggt gct gaa atg			1199
Val Asn Lys Asp Asp Leu Leu Gln Met Val Arg Phe Gly Ala Glu Met			
385	390	395	
ggt ttc agt tct aag gac agc aca ata act gat gag gac att gac cgt			1247
Val Phe Ser Ser Lys Asp Ser Thr Ile Thr Asp Glu Asp Ile Asp Arg			
400	405	410	415
att ata gct aaa gga gag gag aca aca gca gaa ctt gat gcg aaa atg			1295
Ile Ile Ala Lys Gly Glu Glu Thr Thr Ala Glu Leu Asp Ala Lys Met			
	420	425	430
aaa aag ttc act gag gat gcc atc aaa ttt aag atg gat gat aat gct			1343
Lys Lys Phe Thr Glu Asp Ala Ile Lys Phe Lys Met Asp Asp Asn Ala			
	435	440	445
gaa ttg tat gac ttc gat gat gag aag gat gaa aac aag gtt gat ttc			1391
Glu Leu Tyr Asp Phe Asp Asp Glu Lys Asp Glu Asn Lys Val Asp Phe			
	450	455	460
aag aaa ctt gtt agt gat aac tgg att gag cca cct aga aga gaa agg			1439
Lys Lys Leu Val Ser Asp Asn Trp Ile Glu Pro Pro Arg Arg Glu Arg			
	465	470	475
aag nga aac tac tct gag tct tga			1463
Lys Xaa Asn Tyr Ser Glu Ser			
480	485		

<210> 14  
 <211> 486  
 <212> PRT  
 <213> Zea mays

<220>  
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 <222> (0)...(0)  
 <223> Xaa = Any Amino Acid

<400> 14  
 Arg Pro Thr Arg Pro Pro Glu Glu Arg Asn His Ile Arg Asp Asn Leu  
 1 5 10 15  
 Leu Gln Pro Gly Lys Phe Asp Val Cys Val Thr Ser Phe Glu Met Ala  
 20 25 30  
 Ile Lys Glu Lys Ser Ala Leu Arg Arg Phe Ser Trp Arg Tyr Ile Ile  
 35 40 45  
 Ile Asp Glu Ala His Arg Ile Lys Asn Glu Asn Ser Leu Leu Ser Lys  
 50 55 60  
 Thr Met Arg Ile Tyr Asn Thr Asn Tyr Arg Leu Leu Ile Thr Gly Thr  
 65 70 75 80  
 Pro Leu Gln Asn Asn Leu His Glu Leu Trp Ala Leu Leu Asn Phe Leu  
 85 90 95  
 Leu Pro Glu Ile Phe Ser Ser Ala Glu Thr Phe Asp Glu Trp Phe Gln  
 100 105 110





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<222> (1)...(23)

<400> 15
ccagaagagc ggaaccatat aag 23

<210> 16
<211> 23
<212> DNA
<213> Zea mays

<220>
<221> primer_bind
<222> (1)...(23)

<400> 16
ctcttctagg tggctcaatc cag 23

<210> 17
<211> 1645
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (2)...(1642)

<221> misc_feature
<222> (0)...(0)
<223> n = A, T, C, or G; Xaa = Any Amino Acid

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Ala Asp Gly Arg Arg Tyr Met Ile Arg Arg Arg Leu Leu Leu Thr Gly
1 5 10 15

act cct atc caa aac agc ctg caa gag ctc tgg tct ttg ctt aac ttc 97
Thr Pro Ile Gln Asn Ser Leu Gln Glu Leu Trp Ser Leu Leu Asn Phe
20 25 30

atc ctg ccc aat att ttt aat tca tcc cag aat ttt gag gaa tgg ttt 145
Ile Leu Pro Asn Ile Phe Asn Ser Ser Gln Asn Phe Glu Glu Trp Phe
35 40 45

aat gca cca ttt gca tgt gat gtc agt ctt aat gat gag gaa caa cta 193
Asn Ala Pro Phe Ala Cys Asp Val Ser Leu Asn Asp Glu Glu Gln Leu
50 55 60

cta atc ata cat cgt ttg cat caa gtt ttg cgt cca ttc ttg ctg agg 241
Leu Ile Ile His Arg Leu His Gln Val Leu Arg Pro Phe Leu Leu Arg
65 70 75 80

agg aag aaa gat gaa gta nag aaa tat ctc cct gtg aaa aca caa gta 289
Arg Lys Lys Asp Glu Val Xaa Lys Tyr Leu Pro Val Lys Thr Gln Val
85 90 95

att ctc aag tgt gac atg tct gct tgg caa aaa gca tac tac gaa caa 337

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Ile	Leu	Lys	Cys	Asp	Met	Ser	Ala	Trp	Gln	Lys	Ala	Tyr	Tyr	Glu	Gln		
			100					105					110				
gtc	aca	agc	agg	gaa	aag	gtt	gcg	cta	gga	tat	ggg	atc	aga	aag	aag	385	
Val	Thr	Ser	Arg	Glu	Lys	Val	Ala	Leu	Gly	Tyr	Gly	Ile	Arg	Lys	Lys		
		115					120				125						
gct	ctg	caa	aat	ctg	tca	atg	caa	ctt	agg	aag	tgt	tgc	aat	cat	ccc	433	
Ala	Leu	Gln	Asn	Leu	Ser	Met	Gln	Leu	Arg	Lys	Cys	Cys	Asn	His	Pro		
	130					135				140							
tac	cta	ttc	gta	gag	cat	tat	aac	atg	tac	caa	cgg	gag	gaa	ata	gtt	481	
Tyr	Leu	Phe	Val	Glu	His	Tyr	Asn	Met	Tyr	Gln	Arg	Glu	Glu	Ile	Val		
145					150				155						160		
aga	gca	tcc	gga	aag	ttt	gaa	ttg	ctt	gat	cgt	cta	ctt	ccg	aaa	ttg	529	
Arg	Ala	Ser	Gly	Lys	Phe	Glu	Leu	Leu	Asp	Arg	Leu	Leu	Pro	Lys	Leu		
				165					170					175			
cag	aga	gct	ggg	cac	agg	gtt	tta	ctt	ttc	tct	cag	atg	aca	aaa	ttg	577	
Gln	Arg	Ala	Gly	His	Arg	Val	Leu	Leu	Phe	Ser	Gln	Met	Thr	Lys	Leu		
			180					185					190				
ctt	gac	gtt	tta	gaa	ata	tat	ttg	cag	atg	tac	aat	ttc	aag	tac	atg	625	
Leu	Asp	Val	Leu	Glu	Ile	Tyr	Leu	Gln	Met	Tyr	Asn	Phe	Lys	Tyr	Met		
		195					200					205					
agg	ctt	gat	gga	tcc	aca	aag	act	gaa	gaa	cgt	ggg	agg	tta	ctg	gca	673	
Arg	Leu	Asp	Gly	Ser	Thr	Lys	Thr	Glu	Glu	Arg	Gly	Arg	Leu	Leu	Ala		
	210					215					220						
gat	ttt	aat	aag	aag	aat	tca	gaa	tat	ttc	atg	ttt	ctt	ctc	agc	aca	721	
Asp	Phe	Asn	Lys	Lys	Asn	Ser	Glu	Tyr	Phe	Met	Phe	Leu	Leu	Ser	Thr		
225					230				235						240		
cga	gcc	gga	ggg	ctt	gga	ttg	aac	ttg	cag	act	gca	gac	acc	gtc	att	769	
Arg	Ala	Gly	Gly	Leu	Gly	Leu	Asn	Leu	Gln	Thr	Ala	Asp	Thr	Val	Ile		
				245					250					255			
atc	ttt	gat	agt	gac	tgg	aac	cct	cag	atg	gac	caa	caa	gct	gag	gac	817	
Ile	Phe	Asp	Ser	Asp	Trp	Asn	Pro	Gln	Met	Asp	Gln	Gln	Ala	Glu	Asp		
			260					265					270				
cgt	gcc	cat	cgt	ata	ggg	caa	aag	aac	gaa	gta	cgt	gtg	ttt	gtt	ctt	865	
Arg	Ala	His	Arg	Ile	Gly	Gln	Lys	Asn	Glu	Val	Arg	Val	Phe	Val	Leu		
		275					280					285					
gtt	agc	gtt	ggg	tca	att	gaa	gaa	gag	ata	ttg	gat	cgt	gcg	aaa	cag	913	
Val	Ser	Val	Gly	Ser	Ile	Glu	Glu	Glu	Ile	Leu	Asp	Arg	Ala	Lys	Gln		
		290				295					300						
aag	atg	ggg	att	gat	gca	aaa	gta	atc	cag	gct	ggg	ttg	ttt	aac	acg	961	
Lys	Met	Gly	Ile	Asp	Ala	Lys	Val	Ile	Gln	Ala	Gly	Leu	Phe	Asn	Thr		
305					310					315					320		
acc	tcc	aca	gca	cag	gac	agg	cga	gca	ttg	ctg	cag	gag	ata	ctc	agg	1009	

Thr Ser Thr Ala Gln Asp Arg Arg Ala Leu Leu Gln Glu Ile Leu Arg	
325 330 335	
aga gga aca agc tca ctg gga acg gat atc ccc agt gaa cgt gag ata	1057
Arg Gly Thr Ser Ser Leu Gly Thr Asp Ile Pro Ser Glu Arg Glu Ile	
340 345 350	
aac cgc ttg gct gct cga aac gat gaa gaa ttc cgg ttg ttt gag aag	1105
Asn Arg Leu Ala Ala Arg Asn Asp Glu Glu Phe Arg Leu Phe Glu Lys	
355 360 365	
atg gat gaa gaa agg agg cta aag gag aac tac aaa tct aga ctt atg	1153
Met Asp Glu Glu Arg Arg Leu Lys Glu Asn Tyr Lys Ser Arg Leu Met	
370 375 380	
gat gga aat gag gtc cca gat tgg gtg ttt gcc aat gat aat gaa acc	1201
Asp Gly Asn Glu Val Pro Asp Trp Val Phe Ala Asn Asp Asn Glu Thr	
385 390 395 400	
tta cgc aag aaa acc gtg gca gat gaa ttc cgg aat ata att gtt ggt	1249
Leu Arg Lys Lys Thr Val Ala Asp Glu Phe Arg Asn Ile Ile Val Gly	
405 410 415	
tca aag aga cgt aga aag gag gtt gtc tat tcg gac tct ttt ggt gat	1297
Ser Lys Arg Arg Arg Lys Glu Val Val Tyr Ser Asp Ser Phe Gly Asp	
420 425 430	
cag tgg atg aaa tcc gac gag gga ttt gaa gag att gca aag atg act	1345
Gln Trp Met Lys Ser Asp Glu Gly Phe Glu Glu Ile Ala Lys Met Thr	
435 440 445	
cca agg gtg aag cga act gct tat tcg cct gac att caa gtt gag tac	1393
Pro Arg Val Lys Arg Thr Ala Tyr Ser Pro Asp Ile Gln Val Glu Tyr	
450 455 460	
aat gaa agg agg aaa agg ccc aag tct gtg gaa aac agc gca gat ggc	1441
Asn Glu Arg Arg Lys Arg Pro Lys Ser Val Glu Asn Ser Ala Asp Gly	
465 470 475 480	
gca agc aac cca aca cgg aca ccc gac aaa gga agg gct gga gtt tca	1489
Ala Ser Asn Pro Thr Arg Thr Pro Asp Lys Gly Arg Ala Gly Val Ser	
485 490 495	
tca tac agc aag gat gag acc gaa gat gat ggt gaa gac gaa gtc atc	1537
Ser Tyr Ser Lys Asp Glu Thr Glu Asp Asp Gly Glu Asp Glu Val Ile	
500 505 510	
acc agt ggc tta cag aag ggt aac agt ttc aca tgg aag acc ctt gga	1585
Thr Ser Gly Leu Gln Lys Gly Asn Ser Phe Thr Trp Lys Thr Leu Gly	
515 520 525	
aga aaa agg tca agc cac tta agt tcg tcg tcg gac tca aaa ggg cga	1633
Arg Lys Arg Ser Ser His Leu Ser Ser Ser Ser Asp Ser Lys Gly Arg	
530 535 540	
cca tca ttc taa	1645

Pro Ser Phe  
545

<210> 18  
<211> 547  
<212> PRT  
<213> Zea mays

<220>  
<221> VARIANT  
<222> (0)...(0)  
<223> Xaa = any amino acid

<400> 18  
Ala Asp Gly Arg Arg Tyr Met Ile Arg Arg Arg Leu Leu Leu Thr Gly  
1 5 10 15  
Thr Pro Ile Gln Asn Ser Leu Gln Glu Leu Trp Ser Leu Leu Asn Phe  
20 25 30  
Ile Leu Pro Asn Ile Phe Asn Ser Gln Asn Phe Glu Glu Trp Phe  
35 40 45  
Asn Ala Pro Phe Ala Cys Asp Val Ser Leu Asn Asp Glu Glu Gln Leu  
50 55 60  
Leu Ile Ile His Arg Leu His Gln Val Leu Arg Pro Phe Leu Leu Arg  
65 70 75 80  
Arg Lys Lys Asp Glu Val Xaa Lys Tyr Leu Pro Val Lys Thr Gln Val  
85 90 95  
Ile Leu Lys Cys Asp Met Ser Ala Trp Gln Lys Ala Tyr Tyr Glu Gln  
100 105 110  
Val Thr Ser Arg Glu Lys Val Ala Leu Gly Tyr Gly Ile Arg Lys Lys  
115 120 125  
Ala Leu Gln Asn Leu Ser Met Gln Leu Arg Lys Cys Cys Asn His Pro  
130 135 140  
Tyr Leu Phe Val Glu His Tyr Asn Met Tyr Gln Arg Glu Glu Ile Val  
145 150 155 160  
Arg Ala Ser Gly Lys Phe Glu Leu Leu Asp Arg Leu Leu Pro Lys Leu  
165 170 175  
Gln Arg Ala Gly His Arg Val Leu Leu Phe Ser Gln Met Thr Lys Leu  
180 185 190  
Leu Asp Val Leu Glu Ile Tyr Leu Gln Met Tyr Asn Phe Lys Tyr Met  
195 200 205  
Arg Leu Asp Gly Ser Thr Lys Thr Glu Glu Arg Gly Arg Leu Leu Ala  
210 215 220  
Asp Phe Asn Lys Lys Asn Ser Glu Tyr Phe Met Phe Leu Leu Ser Thr  
225 230 235 240  
Arg Ala Gly Gly Leu Gly Leu Asn Leu Gln Thr Ala Asp Thr Val Ile  
245 250 255  
Ile Phe Asp Ser Asp Trp Asn Pro Gln Met Asp Gln Gln Ala Glu Asp  
260 265 270  
Arg Ala His Arg Ile Gly Gln Lys Asn Glu Val Arg Val Phe Val Leu  
275 280 285  
Val Ser Val Gly Ser Ile Glu Glu Glu Ile Leu Asp Arg Ala Lys Gln  
290 295 300  
Lys Met Gly Ile Asp Ala Lys Val Ile Gln Ala Gly Leu Phe Asn Thr  
305 310 315 320  
Thr Ser Thr Ala Gln Asp Arg Arg Ala Leu Leu Gln Glu Ile Leu Arg

Arg	Gly	Thr	Ser	325	Ser	Leu	Gly	Thr	Asp	330	Ile	Pro	Ser	Glu	Arg	335	Glu	Ile
			340						345							350		
Asn	Arg	Leu	Ala	Ala	Arg	Asn	Asp	Glu	Glu	Phe	Arg	Leu	Phe	Glu	Lys			
		355					360						365					
Met	Asp	Glu	Glu	Arg	Arg	Leu	Lys	Glu	Asn	Tyr	Lys	Ser	Arg	Leu	Met			
	370						375					380						
Asp	Gly	Asn	Glu	Val	Pro	Asp	Trp	Val	Phe	Ala	Asn	Asp	Asn	Glu	Thr			
385					390					395					400			
Leu	Arg	Lys	Lys	Thr	Val	Ala	Asp	Glu	Phe	Arg	Asn	Ile	Ile	Val	Gly			
				405						410					415			
Ser	Lys	Arg	Arg	Arg	Lys	Glu	Val	Val	Tyr	Ser	Asp	Ser	Phe	Gly	Asp			
			420						425					430				
Gln	Trp	Met	Lys	Ser	Asp	Glu	Gly	Phe	Glu	Glu	Ile	Ala	Lys	Met	Thr			
		435					440						445					
Pro	Arg	Val	Lys	Arg	Thr	Ala	Tyr	Ser	Pro	Asp	Ile	Gln	Val	Glu	Tyr			
		450				455					460							
Asn	Glu	Arg	Arg	Lys	Arg	Pro	Lys	Ser	Val	Glu	Asn	Ser	Ala	Asp	Gly			
465					470					475					480			
Ala	Ser	Asn	Pro	Thr	Arg	Thr	Pro	Asp	Lys	Gly	Arg	Ala	Gly	Val	Ser			
				485					490						495			
Ser	Tyr	Ser	Lys	Asp	Glu	Thr	Glu	Asp	Asp	Gly	Glu	Asp	Glu	Val	Ile			
			500					505						510				
Thr	Ser	Gly	Leu	Gln	Lys	Gly	Asn	Ser	Phe	Thr	Trp	Lys	Thr	Leu	Gly			
		515					520						525					
Arg	Lys	Arg	Ser	Ser	His	Leu	Ser	Ser	Ser	Ser	Asp	Ser	Lys	Gly	Arg			
	530					535					540							
Pro	Ser	Phe																
545																		

<210> 19  
 <211> 23  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> primer\_bind  
 <222> (1)...(23)

<400> 19  
 acaggcactc ctatccaaaa cag

23

<210> 20  
 <211> 23  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> primer\_bind  
 <222> (1)...(23)

<400> 20  
 gaatgatggt cgcccttttg agt

23

<210> 21  
 <211> 514

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<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (6)...(514)

<221> misc_feature
<222> (0)...(0)
<223> n = A, T, C, or G; Xaa = Any Amino Acid

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      Asn Phe Leu Leu Pro Lys Xaa Xaa Gln Phe His Pro Gly Gly Leu
        1             5             10             15

ctc tca aat ggt tta ata agc cat ttg aga gtg ctt gga gat agc tcg      98
Leu Ser Asn Gly Leu Ile Ser His Leu Arg Val Leu Gly Asp Ser Ser
          20             25             30

cct gat gaa gct tta ntg tcc gag gag gag aat ctc ttg att ata aat      146
Pro Asp Glu Ala Leu Xaa Ser Glu Glu Glu Asn Leu Leu Ile Ile Asn
          35             40             45

cgt ctg cac caa gtt ttg aga cca ttt gta ctt agg agg ctg aaa cac      194
Arg Leu His Gln Val Leu Arg Pro Phe Val Leu Arg Arg Leu Lys His
          50             55             60

aag gtt gaa aat gag ttg cct gag aag att gag aga cta ata aga tgt      242
Lys Val Glu Asn Glu Leu Pro Glu Lys Ile Glu Arg Leu Ile Arg Cys
          65             70             75

gag gcc tca tca tat caa aaa ctt ttg atg aag agg gtg gaa gaa aat      290
Glu Ala Ser Ser Tyr Gln Lys Leu Leu Met Lys Arg Val Glu Glu Asn
          80             85             90             95

ctt ggt tct att ggc aat tca aag gct cga tca gta cac aac tct gtc      338
Leu Gly Ser Ile Gly Asn Ser Lys Ala Arg Ser Val His Asn Ser Val
          100            105            110

atg gag ctt cgt aat ata tgc aat cat cca tat ctc agt cag ctt cat      386
Met Glu Leu Arg Asn Ile Cys Asn His Pro Tyr Leu Ser Gln Leu His
          115            120            125

gca gag gag gtg gat aac ttc ata cct aaa cat tat ctg cca cca att      434
Ala Glu Glu Val Asp Asn Phe Ile Pro Lys His Tyr Leu Pro Pro Ile
          130            135            140

att aga ctt tgt ggg aag ctt gag atg ttg gac cgt tta ttg cca aaa      482
Ile Arg Leu Cys Gly Lys Leu Glu Met Leu Asp Arg Leu Leu Pro Lys
          145            150            155

ttg aag gcg aca gat cat cgg gtt ctt ttc tt                          514
Leu Lys Ala Thr Asp His Arg Val Leu Phe
          160            165

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<210> 22  
 <211> 169  
 <212> PRT  
 <213> Glycine max

<220>  
 <221> VARIANT  
 <222> (0)...(0)  
 <223> Xaa = Any Amino Acid

<400> 22  
 Asn Phe Leu Leu Pro Lys Xaa Xaa Gln Phe His Pro Gly Gly Leu Leu  
 1 5 10 15  
 Ser Asn Gly Leu Ile Ser His Leu Arg Val Leu Gly Asp Ser Ser Pro  
 20 25 30  
 Asp Glu Ala Leu Xaa Ser Glu Glu Asn Leu Leu Ile Ile Asn Arg  
 35 40 45  
 Leu His Gln Val Leu Arg Pro Phe Val Leu Arg Arg Leu Lys His Lys  
 50 55 60  
 Val Glu Asn Glu Leu Pro Glu Lys Ile Glu Arg Leu Ile Arg Cys Glu  
 65 70 75 80  
 Ala Ser Ser Tyr Gln Lys Leu Leu Met Lys Arg Val Glu Glu Asn Leu  
 85 90 95  
 Gly Ser Ile Gly Asn Ser Lys Ala Arg Ser Val His Asn Ser Val Met  
 100 105 110  
 Glu Leu Arg Asn Ile Cys Asn His Pro Tyr Leu Ser Gln Leu His Ala  
 115 120 125  
 Glu Glu Val Asp Asn Phe Ile Pro Lys His Tyr Leu Pro Pro Ile Ile  
 130 135 140  
 Arg Leu Cys Gly Lys Leu Glu Met Leu Asp Arg Leu Leu Pro Lys Leu  
 145 150 155 160  
 Lys Ala Thr Asp His Arg Val Leu Phe  
 165

<210> 23  
 <211> 23  
 <212> DNA  
 <213> Glycine max

<220>  
 <221> primer\_bind  
 <222> (1)...(23)

<400> 23  
 aacccgatga tctgtcgct tca

23

<210> 24  
 <211> 23  
 <212> DNA  
 <213> Glycine max

<220>  
 <221> primer\_bind  
 <222> (1)...(23)



<400> 24  
tcatccagga ggactttctct caa 23

<210> 25  
<211> 403  
<212> DNA  
<213> Glycine max

<220>  
<221> CDS  
<222> (221)...(403)

<221> misc\_feature  
<222> (0)...(0)  
<223> n = A, T, C, or G

<400> 25  
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cnaatgaatca agtgattgnt attttatttc atgtgtcacc cagccatatt ggcagatgaa 120  
atgggtcttg gcaaaacagt tcaggtagct attctgtttt ttattatttt aatatgttct 180  
ntaatttggt tgtnttccta atcctttact tttcaagtaa gaa atg cca tat gtt 235  
Glu Met Pro Tyr Val  
1 5

ctt gtc ttc cag gcc atc aca tat tta act ttg ctg aaa cac ttg cac 283  
Leu Val Phe Gln Ala Ile Thr Tyr Leu Thr Leu Leu Lys His Leu His  
10 15 20

aat gat tct ggt cca cat ctt ata gta tgt cct gct tct gtt ctg gaa 331  
Asn Asp Ser Gly Pro His Leu Ile Val Cys Pro Ala Ser Val Leu Glu  
25 30 35

aac tgg gaa agg gaa tta aaa agg tgg tgt cca tcc ttt tct gtt ctt 379  
Asn Trp Glu Arg Glu Leu Lys Arg Trp Cys Pro Ser Phe Ser Val Leu  
40 45 50

caa tac cat ggg gcc gga cgt gca 403  
Gln Tyr His Gly Ala Gly Arg Ala  
55 60

<210> 26  
<211> 61  
<212> PRT  
<213> Glycine max

<220>  
<221> VARIANT  
<222> (0)...(0)  
<223> Xaa = Any Amino Acid

<400> 26  
Glu Met Pro Tyr Val Leu Val Phe Gln Ala Ile Thr Tyr Leu Thr Leu  
1 5 10 15  
Leu Lys His Leu His Asn Asp Ser Gly Pro His Leu Ile Val Cys Pro  
20 25 30

Ala Ser Val Leu Glu Asn Trp Glu Arg Glu Leu Lys Arg Trp Cys Pro  
35 40 45  
Ser Phe Ser Val Leu Gln Tyr His Gly Ala Gly Arg Ala  
50 55 60

<210> 27  
<211> 23  
<212> DNA  
<213> Glycine max

<220>  
<221> primer\_bind  
<222> (1)...(23)

<400> 27  
gccccatggt attgaagaac aga 23

<210> 28  
<211> 25  
<212> DNA  
<213> Glycine max

<220>  
<221> primer\_bind  
<222> (1)...(25)

<400> 28  
atattatttc atgtgtcacc cagcc 25

<210> 29  
<211> 522  
<212> DNA  
<213> Oryza sativa

<220>  
<221> CDS  
<222> (1)...(522)

<221> misc\_feature  
<222> (0)...(0)  
<223> n = A, T, C or G; Xaa = Any Amino Acid

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Val Ser Gly Arg Lys Ala Gln Tyr Ser Lys Lys Asn Ser Arg Asn Val  
1 5 10 15

gat tca ctc cct ttg atg gag ggt gaa ggg cgt gct tta aaa gtt tat 96  
Asp Ser Leu Pro Leu Met Glu Gly Glu Gly Arg Ala Leu Lys Val Tyr  
20 25 30

gga ttc aat cac gtt caa cga aca caa ttc cta cag aca ctc atg agg 144  
Gly Phe Asn His Val Gln Arg Thr Gln Phe Leu Gln Thr Leu Met Arg  
35 40 45

tat ggt ttt cag aac tat gat tgg aaa gag tat ctt cct cgt ttg aag 192

Tyr	Gly	Phe	Gln	Asn	Tyr	Asp	Trp	Lys	Glu	Tyr	Leu	Pro	Arg	Leu	Lys		
	50					55					60						
ggg	aaa	agt	gtt	gag	gaa	att	cag	aga	tat	ggt	gag	ctt	gtc	atg	gcc	240	
Gly	Lys	Ser	Val	Glu	Glu	Ile	Gln	Arg	Tyr	Gly	Glu	Leu	Val	Met	Ala		
	65				70				75					80			
cat	ctt	gta	gag	gac	aca	aat	gac	tca	cca	acc	tat	gca	gat	ggt	gtg	288	
His	Leu	Val	Glu	Asp	Thr	Asn	Asp	Ser	Pro	Thr	Tyr	Ala	Asp	Gly	Val		
				85				90						95			
ccg	aag	aaa	tgc	gtg	ctg	atg	aga	cat	tgg	tca	ggc	tag	cca	aaa	tat	336	
Pro	Lys	Lys	Cys	Val	Leu	Met	Arg	His	Trp	Ser	Gly	*	Pro	Lys	Tyr		
			100					105						110			
cac	ttg	tgg	agg	aga	agg	tgg	tgc	atg	gag	caa	gga	aaa	tta	caa	aac	384	
His	Leu	Trp	Arg	Arg	Arg	Trp	Cys	Met	Glu	Gln	Gly	Lys	Leu	Gln	Asn		
			115					120					125				
tct	tcc	cca	act	act	tga	tgt	atg	aat	tta	ctg	gct	tat	cag	gtg	gaa	432	
Ser	Ser	Pro	Thr	Thr	*	Cys	Met	Asn	Leu	Leu	Ala	Tyr	Gln	Val	Glu		
		130						135					140				
gaa	tat	gga	aag	ggg	aac	atg	atc	tac	tgt	nac	tga	agc	ata	ata	agc	480	
Glu	Tyr	Gly	Lys	Gly	Asn	Met	Ile	Tyr	Cys	Xaa	*	Ser	Ile	Ile	Ser		
		145					150						155				
acg	ggt	tgc	cag	tgg	cat	aca	tat	cag	atn	cag	aga	tac	ggg			522	
Thr	Gly	Cys	Gln	Trp	His	Thr	Tyr	Gln	Xaa	Gln	Arg	Tyr	Gly				
		160					165					170					

<210> 30  
 <211> 171  
 <212> PRT  
 <213> Oryza sativa

<220>  
 <221> VARIANT  
 <222> (0)...(0)  
 <223> Xaa = Any Amino Acid

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1				5					10					15		
Asp	Ser	Leu	Pro	Leu	Met	Glu	Gly	Glu	Gly	Arg	Ala	Leu	Lys	Val	Tyr	
			20					25					30			
Gly	Phe	Asn	His	Val	Gln	Arg	Thr	Gln	Phe	Leu	Gln	Thr	Leu	Met	Arg	
		35				40					45					
Tyr	Gly	Phe	Gln	Asn	Tyr	Asp	Trp	Lys	Glu	Tyr	Leu	Pro	Arg	Leu	Lys	
	50				55					60						
Gly	Lys	Ser	Val	Glu	Glu	Ile	Gln	Arg	Tyr	Gly	Glu	Leu	Val	Met	Ala	
65				70					75					80		
His	Leu	Val	Glu	Asp	Thr	Asn	Asp	Ser	Pro	Thr	Tyr	Ala	Asp	Gly	Val	
			85					90						95		
Pro	Lys	Lys	Cys	Val	Leu	Met	Arg	His	Trp	Ser	Gly	Pro	Lys	Tyr	His	

				100					105					110		
Leu	Trp	Arg	Arg	Arg	Trp	Cys	Met	Glu	Gln	Gly	Lys	Leu	Gln	Asn	Ser	
				115				120					125			
Ser	Pro	Thr	Thr	Cys	Met	Asn	Leu	Leu	Ala	Tyr	Gln	Val	Glu	Glu	Tyr	
				130			135				140					
Gly	Lys	Gly	Asn	Met	Ile	Tyr	Cys	Xaa	Ser	Ile	Ile	Ser	Thr	Gly	Cys	
145					150					155					160	
Gln	Trp	His	Thr	Tyr	Gln	Xaa	Gln	Arg	Tyr	Gly						
				165				170								

aaa agg aaa cgg agc aag cta aca gtt agt cca tca agt gag cat gat	193
Lys Arg Lys Arg Ser Lys Leu Thr Val Ser Pro Ser Ser Glu His Asp	
50 55 60	
gct tcc tca cca ata ctg gat tct caa atg aac aat ggc tcc atc aaa	241
Ala Ser Ser Pro Ile Leu Asp Ser Gln Met Asn Asn Gly Ser Ile Lys	
65 70 75 80	
aag aag atc aaa cat gac act aac att tct cca tca acc aag aag ata	289
Lys Lys Ile Lys His Asp Thr Asn Ile Ser Pro Ser Thr Lys Lys Ile	
85 90 95	
aga gga cat gac ggg tac ttc tac gag tgt gta gaa tgt gat ctc ggt	337
Arg Gly His Asp Gly Tyr Phe Tyr Glu Cys Val Glu Cys Asp Leu Gly	
100 105 110	
ggc aat ttg ctg tgc tgt gat agc tgt cca cga aca tac cac ttg gaa	385
Gly Asn Leu Leu Cys Cys Asp Ser Cys Pro Arg Thr Tyr His Leu Glu	
115 120 125	
tgt ctt aat cct cct ctc aag cgt gca cca cct gga aat tgg caa tgc	433
Cys Leu Asn Pro Pro Leu Lys Arg Ala Pro Pro Gly Asn Trp Gln Cys	
130 135 140	
cca aga tgt cgt aca aaa aaa gtt agc ttg aag ctc tta aac aat gct	481
Pro Arg Cys Arg Thr Lys Lys Val Ser Leu Lys Leu Leu Asn Asn Ala	
145 150 155 160	
gat gct gac acc tcc taa acg tga aag aa	510
Asp Ala Asp Thr Ser * Thr * Lys	
165	

<210> 34  
 <211> 167  
 <212> PRT  
 <213> Oryza sativa

<400> 34

Leu Gln Asp Phe Gly Gly Gly Gly Cys Gly Cys Leu Glu Arg Arg Gly	
1 5 10 15	
Leu Ile Ala Thr Ala Cys Asp Val Asp Thr Leu Met Met Lys Glu Arg	
20 25 30	
Ser Ser Leu Cys Glu Ser Ala Ala Asp Gly Ser Trp Val Leu Lys Tyr	
35 40 45	
Lys Arg Lys Arg Ser Lys Leu Thr Val Ser Pro Ser Ser Glu His Asp	
50 55 60	
Ala Ser Ser Pro Ile Leu Asp Ser Gln Met Asn Asn Gly Ser Ile Lys	
65 70 75 80	
Lys Lys Ile Lys His Asp Thr Asn Ile Ser Pro Ser Thr Lys Lys Ile	
85 90 95	
Arg Gly His Asp Gly Tyr Phe Tyr Glu Cys Val Glu Cys Asp Leu Gly	
100 105 110	
Gly Asn Leu Leu Cys Cys Asp Ser Cys Pro Arg Thr Tyr His Leu Glu	
115 120 125	
Cys Leu Asn Pro Pro Leu Lys Arg Ala Pro Pro Gly Asn Trp Gln Cys	

130	135	140	
Pro Arg Cys Arg Thr Lys Lys Val Ser Leu Lys Leu Leu Asn Asn Ala			
145	150	155	160
Asp Ala Asp Thr Ser Thr Lys			
	165		

<210> 35  
 <211> 23  
 <212> DNA  
 <213> Oryza sativa  
  
 <220>  
 <221> primer\_bind  
 <222> (1)...(23)  
  
 <400> 35  
 cttacaggat ttcgggggag gtg 23  
  
 <210> 36  
 <211> 23  
 <212> DNA  
 <213> Oryza sativa  
  
 <220>  
 <221> primer\_bind  
 <222> (1)...(23)  
  
 <400> 36  
 ctttcacggt taggaggtgt cag 23  
  
 <210> 37  
 <211> 667  
 <212> DNA  
 <213> Triticum aestivum  
  
 <220>  
 <221> CDS  
 <222> (2)...(667)  
  
 <221> misc\_feature  
 <222> (0)...(0)  
 <223> n = A, T, C, or G; Xaa = Any Amino Acid  
  
 <400> 37  
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 Leu Thr Gly Thr Pro Leu Gln Asn Asn Ile Gly Glu Met Tyr Asn Leu  
 1 5 10 15  
  
 ttg aac ttc cta cag cct gct tct ttc cct tct cta gca tca ttt gag 97  
 Leu Asn Phe Leu Gln Pro Ala Ser Phe Pro Ser Leu Ala Ser Phe Glu  
 20 25 30  
  
 gag aag ttt aat gaa ctt gca aca gca gag aaa gtg gag gag ctg aag 145  
 Glu Lys Phe Asn Glu Leu Ala Thr Ala Glu Lys Val Glu Glu Leu Lys  
 35 40 45

aaa ctg gta gca cca cat atg ctt cga agg ctg aaa aaa gat gca atg Lys Leu Val Ala Pro His Met Leu Arg Arg Leu Lys Lys Asp Ala Met 50 55 60	193
aaa aat atc ccc ccg aag aca gag cga atg gtg cct gtc gaa ctg aca Lys Asn Ile Pro Pro Lys Thr Glu Arg Met Val Pro Val Glu Leu Thr 65 70 75 80	241
tca atc cag gct gaa tac tac cgt gct atg ctt aca aag aac tac caa Ser Ile Gln Ala Glu Tyr Tyr Arg Ala Met Leu Thr Lys Asn Tyr Gln 85 90 95	289
gta ctg cgt aat acc gga aaa ggt ggt gct cat cag tca ttg ctc aat Val Leu Arg Asn Thr Gly Lys Gly Gly Ala His Gln Ser Leu Leu Asn 100 105 110	337
ata gta atg cag ctt cgg aaa ttt gca acc atc cat atc tta tcc tgg Ile Val Met Gln Leu Arg Lys Phe Ala Thr Ile His Ile Leu Ser Trp 115 120 125	385
gaa ctg aac ccg aat caa gtt cac cag att ttt gca tga aat gag aat Glu Leu Asn Pro Asn Gln Val His Gln Ile Phe Ala * Asn Glu Asn 130 135 140	433
aaa ggc tca aca aat taa ctt tgt tgc att cta tgc tca aag tgt tac Lys Gly Ser Thr Asn * Leu Cys Cys Ile Leu Cys Ser Lys Cys Tyr 145 150 155	481
aca gtg atg ggc atc gtg ttc taa ttt tcc aga tga cta aac tct tga Thr Val Met Gly Ile Val Phe * Phe Ser Arg * Leu Asn Ser * 160 165 170	529
cat ccc gaa gat anc gac ccg gaa ttg gca taa aca ntn aaa gag naa His Pro Glu Asp Xaa Asp Pro Glu Leu Ala * Thr Xaa Lys Glu Xaa 175 180 185	577
tgg tcg tgt cgt ggg tga cnc aag cac ata nct tca aca gaa ana cgt Trp Ser Cys Arg Gly * Xaa Lys His Ile Xaa Ser Thr Glu Xaa Arg 190 195 200	625
ttg att tgt aca acg gca tgc ntg tat tga cna nac gta can Leu Ile Cys Thr Thr Ala Cys Xaa Tyr * Xaa Xaa Val Xaa 205 210	667

<210> 38  
 <211> 214  
 <212> PRT  
 <213> Triticum aestivum

<220>  
 <221> VARIANT  
 <222> (0)...(0)  
 <223> Xaa = Any Amino Acid

<400> 38

Leu Thr Gly Thr Pro Leu Gln Asn Asn Ile Gly Glu Met Tyr Asn Leu  
 1 5 10 15  
 Leu Asn Phe Leu Gln Pro Ala Ser Phe Pro Ser Leu Ala Ser Phe Glu  
 20 25 30  
 Glu Lys Phe Asn Glu Leu Ala Thr Ala Glu Lys Val Glu Glu Leu Lys  
 35 40 45  
 Lys Leu Val Ala Pro His Met Leu Arg Arg Leu Lys Lys Asp Ala Met  
 50 55 60  
 Lys Asn Ile Pro Pro Lys Thr Glu Arg Met Val Pro Val Glu Leu Thr  
 65 70 75 80  
 Ser Ile Gln Ala Glu Tyr Tyr Arg Ala Met Leu Thr Lys Asn Tyr Gln  
 85 90 95  
 Val Leu Arg Asn Thr Gly Lys Gly Gly Ala His Gln Ser Leu Leu Asn  
 100 105 110  
 Ile Val Met Gln Leu Arg Lys Phe Ala Thr Ile His Ile Leu Ser Trp  
 115 120 125  
 Glu Leu Asn Pro Asn Gln Val His Gln Ile Phe Ala Asn Glu Asn Lys  
 130 135 140  
 Gly Ser Thr Asn Leu Cys Cys Ile Leu Cys Ser Lys Cys Tyr Thr Val  
 145 150 155 160  
 Met Gly Ile Val Phe Phe Ser Arg Leu Asn Ser His Pro Glu Asp Xaa  
 165 170 175  
 Asp Pro Glu Leu Ala Thr Xaa Lys Glu Xaa Trp Ser Cys Arg Gly Xaa  
 180 185 190  
 Lys His Ile Xaa Ser Thr Glu Xaa Arg Leu Ile Cys Thr Thr Ala Cys  
 195 200 205  
 Xaa Tyr Xaa Xaa Val Xaa  
 210

<210> 39  
 <211> 23  
 <212> DNA  
 <213> Triticum aestivum

<220>  
 <221> primer\_bind  
 <222> (1)...(23)

<400> 39  
 gttgactgga accccattac aga

23

<210> 40  
 <211> 23  
 <212> DNA  
 <213> Triticum aestivum

<220>  
 <221> primer\_bind  
 <222> (1)...(23)

<400> 40  
 catgccgttg tacaaatcaa acg

23

<210> 41  
 <211> 12561  
 <212> DNA



<213> Zea mays

<220>

<221> misc\_feature

<222> (1)...(12561)

<223> Zmpk1 genomic sequence

<221> misc\_feature

<222> (0)...(0)

<223> n = A, T, C, or G

<400> 41

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tgcaagctat	ggcaagagct	catcgcttag	gacagactag	taaggatatt	taccttacac	180
tttatattgt	ataaaaaaac	agattttcaa	taagttttgt	ggtgatttta	taattttcat	240
ctgtttttct	tttaggtgat	gatatacagg	cttgtagacc	gaggtacaat	tgaggagcga	300
atgatgcagc	ttacaaaaaa	gaagatttta	ttggagcact	tagttgttgg	tcgactcacc	360
aaagctaata	atgtcaatca	ggtatgttga	ctacttttta	atggtgaatt	ttgtaaacca	420
tcaacttagg	ttgatctttt	atggcctaag	ctatttatga	attcatttat	ggattgaggg	480
ttgagtagtt	acatgttact	ccctccattt	tttatatttg	tgggtgttta	gttcaaaaat	540
aaactaacgg	gtgacaaata	ttcgagaacg	gaggtagtac	tagtaccttc	tgtctgggat	600
gacatgaaat	gaatgtagca	tctgttagta	tcatgtccat	ttctttgtgt	tacattttac	660
aaggcttaaa	accttacaca	tattgccgga	gttggtgact	atttagtctt	atctgtaaatt	720
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tagcatgtgt	gccatatagg	tttagctccg	ctgatgtgtt	atgcacttat	aattcagacc	840
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atattcataa	tctatgtgca	tgcattagtc	cagatcaggc	tgggtgatct	ggtgggcatt	960
ggtacatgca	tggctgaata	agagtttgat	gaccaagggg	aaggcacccc	acatctactc	1020
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gatcatggat	gcaaatctag	aattctagag	ataattagta	tgtatgccct	accaagtagg	2160
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gaataaagtt	gatgagccat	actacgaagc	tatgggagag	agttatcgag	catcgagagg	3060
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actagtcaact	agtgtttgaa	caagtcatgt	gaacacaaat	gacttactga	ttagagtagg	3300
gctacatcag	gggtcaacct	tgagctctta	cctttttgcc	ttggtgatgg	atgagggtcac	3360
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tgtggcggga	gactctagag	tccaaagggt	ttagactcaa	tagaaactaaa	actgaataca	3540
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Val	Leu	Glu	Ala	Pro	Arg	Glu	Asp	Ser	Ser	Ser	Thr	Glu	Pro	Arg	Ser
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Lys	Lys	Met	Glu	Arg	Tyr	Leu	Ile	Lys	Trp	Lys	Gly	Leu	Ser	Tyr	Ile
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